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AUTHORS Bos taurus growth ho untranslated region. AF126288 Ge, W. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea AF125288.1 G1:4894683 Davis, M.E., Hines, H.C. 349 bp DNA linear MAM 27-MAY 1999 growth hormone receptor (GHK) gene, promoter and 5' to 349) Bos. and itvin, N.M. Bovoidea;

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                                                                                                                                          Submitted (02-JAN-1998) Animal Science, University of Missouri, 164 ASRC, Columbia, MO 65211, USA
                                                                                                                                                                                                                            Unpublished
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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U15731
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Mammalia; Eutheria; Cetartiodaetyla; Ruminantia; Pecora; Hovoidea;
Bovidae; Bovinae; Bos.
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Rapid communication: nucleotide sequence of the promoter and first
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/db_xref="taxon:9913"
/clone+"13-1"
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570. .>732
                                                                                                                                      10257.
                                                                                                                                                                       /rpt_type-tandem
10232...10237
                                                                                                                                                                                                        /note-"liver-specific"
10136. .10175
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                           /note="growth hormone receptor; somatotropin receptor"
                                                                   /number-
                                                                                 /note-"liver-specific"
                                                                                                                  /product-"growth hommone receptor"
                                                                                                                                                      /note="putative"
                                                                                                                                                                                                                                        /tissue_type="liver"
9763. .10256
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                  10258
                                                                                                                                                                                                                                                                             /sex-"male"
                                                                                                                                                                                                                                                                                                                                                  . 25688
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                                                                                                       .10465
                                                    .10392
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Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                  1023-1034 (2001)
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RESULT 4
AL451106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 STRUTTETANTOTTTTTTTTSTTACCAGG 2F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human DNA sequence from allow Epilisian at the mistre XHELX412 Contains the 5' and of the ARHONES gene for odd42 guardine exchange factor 9 (collybistin, FDM 2, HPBM-2, KIAA0121) ESTS, COSS and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either forble-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the
                                                                                                                                                                                                                                                      http://www.samuer.ac.uk/HRP/ChrX
RPII-151A2 is from the library RPOI II.1 constructed by the group
of Pieter de Jong. For turther details see
                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome x, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers give in the feature table with their source databases. En. EMBL. Sw., coursespoon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Jul 17, 2001 this sequence version replaced gi:13751499. During sequence assembly data is compared from overlapping clones, where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24 SEP 2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac ak Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota Metazoa Chordata Craniata Vertebrata Eurole
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 126837)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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AL451106.9 GI:14801108
                                                                                                   Genome Research, 320 Charles Street, Cambridge, MA 02141, HSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt SWISSPROT};\ {\tt Tr:},\ {\tt TREMBL};\ {\tt Wp:},\ {\tt WORMPEP};\ {\tt Information}\ {\tt on}\ {\tt the}\ {\tt WORMPEP}\ {\tt database}\ {\tt can}\ {\tt be}\ {\tt found}\ {\tt at}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEM-2
RP11-151A2 It may be shorter because we sequence overlapping
                                                                        http://www-seq.wi.mit.edu
                                                                                                                                                                 Draft Sequence Produced by Whitehead Institute/MIT Center
                                                                                                                                                                                                   VECTOR: PHACES 6
                                                                                                                                                                                                                              http://www_cheri erg/bacpac/home_htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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25670. .>25688
/codon_start-1
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5982 c 6005 g :
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/protein_id="AAK31298.1"
/db_xrof="G1:[3572470"
                              This sequence is not the entire insert of clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 26; DB 4
100.0%; Pred, No. 0.24;

    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
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27. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"MIR repeat: matches 63. .148 of consensus" 8033. .8210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /nute-"MIR repeat. matches 45, .146 of consensus" 6055, .6155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"match: GSS: Em:AQ098555" 4392. .4882
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                    match: cDNAs: Em:AB007884 match: bSTs: Em:AB007884 match:
                                                           (collybistic, PEM-2, HPEM-2, KIAA0424))
/note="continues as bA570J18.1.mRNA in bA35703.2.mRNA in Em:AL391277
                                                                                                                                                                                                                                                          complement(<14719. .15600)
/gene-"AkhGEF9"
                                                                                                                                                                                                                                                                                                                     /note="18 copies 2 mer aa 86% conserved" complement(14719. .45669)
                                                                                                                                                                                                                                                                                                                                                                     /hote="MIR repeat. matches 106. .192 of conscisus"
12845. .12880
                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluSx repeat: matches 1.
10109. .10200
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3698. .3970
/evidence=not_experimental
                                                                                                 /product *bal5la2.1 (Cdc42 quantite exchange factor (GEF) 9 (collybistic, PEM-2, HPEM-2, NIAA0424))
                                                                                                                                                                    /evidence-not_experimental
complement(<14791. .15600)</pre>
                                                                                                                                                                                                               /product="bA151A2.1 (Cdc42 guanine exchange factor (GEF)
(ccilybistin, FEM-2, HPEM-2, KIAA8434))"
                                                                                                                                                                                                                                                                                                     /gene-"ARHGEF9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"MER5B repeat: matches 8. .175 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Mik repeat; matches 36. .146 of consensus"
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/elone_lib~"RPC1-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome-"X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                               /gene-"AKHGEF9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "match. GSS. Em.AQ460321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat: matches 2652. .2708 of consensus*
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                                                                                                                                                                                                                                                                                                                                                                                                                                   .310 of consensus*
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protein_id="CACB8407.1"
/db_xret="Gd-15848925"
/translation=""""""
  29078. (29445
Colloca THEDIC COPPUT (matched 3)
                                                                                                                                                                                                                                           complement (27531. .28072)
                                                                                                                                                                                                                                                                                                                                 complement (27269. ,27707)
/gene-"ARHCFF9"
                                                                                                                                                                                                                                                                                                                                                                                                  26480. .20749
/hister "12 repeat: matches 2499. .2750 of consensus"
complement(27245. .27708)
/dene-"ARHIGEP9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24359. .24460
Zoole-"MIR gepeat matches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"MIR repeat; matches 57, .105 of consensus" 21770, .21932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /hole "MIR repeat, matches 20, 21724, 21772
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/hoto "12 repeat. Matches 1244. .2100 of conscisus"
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/order "polluler Lodoua 2, alternativel, splined in STOIR
match: EST4: Fm:AIZ91104 Em:BEZ18320 Em:AI301971*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(<14909. .15163,15408. .15588))
/deno-"ARHODEG"
                                                          /note-"LIPH2 repeat: matches 5548. .6155 of consensus"
                                                                                                                                  /note="MIR repeat: matches 148. .241 of consensus" 28319. .28474
                                                                                                                                                                            /note-"match: GSS: Em:AQ775924"
28088. .28181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-*LIPAIO repeat: matches 5203. .6153 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"TIGGER2 repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"12 repeat. matches 2568, ,2758 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"MIR repeat: matches 50. .117 of consensus"
20156. .20420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16807
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16516. .16647
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15321. .15825
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                                                                                      /note-"match: GSS: Em:AE046289"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mote="TIGGER2 repeat; matches 2273, .2715 of consensus"
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19563, 19629
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                                                                                                                                                                                                                      *ARHGEF9*
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REFERENCE

JOURNAL AUTHORS

> Direct Submission Worley, K.C

(bases i to 164427)

Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, barlor college of Medicine, One Baylor Plaza, Houston, TX 77030, USA

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                         Feery,J., Ferez.L., Feters,L., Fickens,R., Frimus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojabokan,I., Rolle,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Store,H., Sutton,A., Svatte,A., Jabo,F., Jamerisa,A., Jamerisa,K., Tana,H., Tansey,J., Taylor,C., Taylor,T., Telirod,B., Thomas,N., Thomas,S., Osman,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Malling, G., Washington,C., Washingt
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Bowle,S., Brieva,M., Brown,E., Brown,M., Bryan,C., P., Buhay,C.,
Burset,M., Carron,T.E.,
Burset,M., Cavazos,S.R., Chacko,J., Charez,D., Chen,G., Chen,R.,
Carter,M., Cavazos,S.R., Chacko,J., Charez,D., Chen,G., Chen,R.,
Unpublished
                                                                                                                                                                                                                                                                    Watlington,S., Williams.G., Williamsen,A., Wleezyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
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                                                                                             Direct Submission
                                                                                                                                                                                                   Weinstock, G. and Gibbs, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
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Mizny, D.M., Adams, C., Adio-eduola, B., Ali-esman, F.R., Allen, C., Argale, M., Banks, T., Alsbrecks, S.L., Amaratunqe, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benlon, J., Pimage, K., Blankenburg, K., Deonin, D., Bouck, J., Bowle, S., Rrieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bowle, S., Rrieva, M., Brown, E., Brown, M., Bryant, N.P., Buthay, C., Burch, P., Burkett, C., Burrell, K.L., Prd, N.C., Carter, M., Cavaros, S.F., Chacke, J., Chayer, C., Chen, C., Chen, Z., Chowdhry, J., Christopoulos, C., Chen, C., Coyle, M.D., Dahorne, S.R., David, R., Develand, C.D., Cox, C., Coyle, M.D., Dahorne, S.R., David, R., Develand, C.D., Cox, C., Coyle, M.D., Dahorne, S.R., David, R., Delandey, K.R., Delando, O., Denn, A.L., Ding, Y., Dinh, H.H., Denneth, R., De
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10 JUL-2002) Buman Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Haylor Plaza, Houston, TX 77030, USA
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                                                          Contact: hqsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                      Center: Baylor College of Medicine
                                                                                                                                                       Web site: http://www.hpa-lentin-wdo/
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    arbitrary, Gaps between the configs are represented as
    runs of N. but the exact sizes of the gaps are unknown.
    This record will be updated with the finished sequence.

    (see http://www.ipsc.ton.fr.deg.d.s, Genbank_draft_data.html).
    NOTE: This is a 'working draft' sequence. It currently
    consists of 58 contigs. The true order of the preces
    is not known and their order in this sequence record is

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ★ as soon as it is available and the accession number will
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    be preserved.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: GCWC
Center clone name: CH230-8J1
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44405
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20991: contiq of
21091: gap of
22202:
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26834:
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29857;
          44404: gap of unknown length
42001: contig of 2597 bp in length
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4091: costia of 1451 bp in length
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2540: contig of 1244 bp in length
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3: contig of 1496 bp in length

3: gap of unknown length

7: contig of 1427 bp in length

7: gap of unknown length

3: contig of 1673 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                    2: gap of unknown length
is contig of 1724 bp in length
is gap of unknown length
le contig of 2045 bp in length
leap of unknown length
costig of 1111 bp in length
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contig of 2909 bp in length
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contig of 1717
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contig of 2286
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contig of 2046
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contig of 2193 bp in length
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contig of 1734 bp in
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g of 1432
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of 1731
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of 1144 bp in length
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bp in length

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AC101881/c
                                                                   Matches
                                                                                   Query Match
                                 80065 GTGCTTTAATCTTTCCTGGAATCAGG 80040
                                                                            Local
                                           1 GTGCTCTAATCTTTTCTGGTACCAGG
                                                                            Similarity
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163131
173436
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155748
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147573
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AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                               JUKNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                    INTERNAL
                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                    3 (bases 1 to 198624)
Birren, B., Nusbaum, C., Lander, E.,
                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                             Jones, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hagos,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ginde,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren, B., Nusbaum, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
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ACTOTART TORKETS TO THE WAS MUSICALLY CITED OF THE SEQUENCE.
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                        21-AUG-2002
                                                                                                 unordered
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Mus musculus, clone RP23-387F19 Metazoa; Chordata; Craniata; Verfebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus and Lander, E

Lamazares, R., Landers, T., Lebuczky, J., Levine, R., Liu, G.,
MacLean, C., Macdenaid, F., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPhetters, R., Melorim, J.,
Mcneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nayee, C.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesiaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Triqillo, J., Vassilee, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zinmer, A., and Zody, M. Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Loquslavkiy,L., Boukhqalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Chepet,Y., Culadgelo,M., Cullins,S., Cullymore,A., Cook,A., Cooke,F., Pearellano,K., Ewat,K., Elan,J.C., Budje,S., Faro,S., Ferreira,P., FitcHugh,W., Gage,D., Galagan,J., Gardyna,S., FitcHugh,W., Galagan,J., FitcHugh,W., Galagan,B., FitcHugh,W., Kamat, A., Karatas, A., Kells, C., LaRocque, K Goyette,M., Graham,L., Grand-Pierre,N., A., Horton,L., Hulme,W., Iliev,I., Johns Johnson, R.,

Submitted (23-NoV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Karatas, A., Kells, C., Handers, T., Hevine, K., Hindbiad-Onlon, N., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mibova, T., Mienga, V., McCarthy, T., Naylor, J., Nayler, C., Nicol, R., Norbu, C., Norman, G.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, F., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, G., Speccer, B., Stange-Thomann, N., Stojancvic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Yound, G., Zainoun, J., Nater C., Simmer, A., and Zody, M. Harna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chaasro,B., Choepe('Y', Collymore,A., Cook A., Chike, P., FeAkellauo,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardynu,S., Gold,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Illev,L., Johnson,R., Jones,C., Kamat,A., Karadas,A., Keils,C., Landers,L., Levine,E., Lindblad-Toh,N., Ali, A., Allen, N., Anderson, S

Followitted (aliant 2002) whitehold listitute, MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced qi:17060657. All repeats were identified using RepeatMasker: Smit, A.F.A. 6 Green, P. (1996-1997) http://flp.gonome.washington.edu/PM/NoppoatMasker.html Contact: sequence_submissions@genome.wi.mit.edu ----- Project Information Center, Whitchead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Genome Center

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ORIGIN
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Db 183534 GOGGICTAATCTTATCTACTACCATG 183509
                                                                                                                                                                                                                             BASE COUNT
                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Source
                                                 1 GTGCTCTAATCTTTTCTGGTACCAGG 26
                                                                                                  22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence, it currently 
* consists of 8 contigs. The true order of the pieces 
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * arbitiar, Sapa between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown 
* This record will be updated with the finished sequence
                                                                                                                                                                                                                       vector_side:right" 62240 i 41171 c 39766 g 54743 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 194000, agarose-tp
Insert size: 197924; sum-of-contigs
Quality coverage: 9.2 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Bye-terminator Biq Dye; 100% of reads Assembly program: Phrap; version 0.960741 Consensus quality: 195624 bases at least 040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 197149 bases at least Q30 Consensus quality: 197644 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conter clone name: 387_F_19
Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145377 135476: qap of 100 bp
185477 171548: contig of 36072 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112420 112519: gap of 100 bp
112520 135176: contid of 22857 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 9.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: Plasmid; n/a; 190% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171549 171648: gap of 100 hp
171649 198624: contig of 26976 bp in longth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98533 98632; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97373 97472: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96511 96610: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95763 95862; gap of
                                                                                                                                                                                                                                                                         /note-*assembly_tragment
clone_end:T7
                                                                                                                                                                                                                                                                                                                             171649. .198624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95863.
                                                                                                                                                                                                                                                                                                                                                                         /note-"assembly_tragment"
135477. .171548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"assembly_fragment"
98633. .112419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector_side:left.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xret="taxon:10090"
/clone="RP29_387F19"
                                                                                                                                                                                                                                                                                                                                               /note-"assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_tragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rlama_lih="wbd1-21 Fomale Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /orqanism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .95\overline{7}62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98532: countid of 1060 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96510; contig of 648 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97372: config of 762 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95762: contig of 95762 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 985 12
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                                                                                                0; Mismatches
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                                                                                                4; Indels
                                                                                                                                                                                                                          704 of hers
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SOCOR
                                                                                                                                                                                        Db 17578 TCTAATCTTTTCTGGTGCCAG 17598
                                                           U82207/c
                                                                                               RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
                                                                                                                                                                                                                                                                                                                                                       Hest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Source
                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                       5 TCTAATCTTTTCTGGTACCAG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
Al.158049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL: Mp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sarape.id=.uk,Tr; jorts,T__ingans,wormpep this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Aiu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (39 SEF 2000) Sanger Centre, Hinxton, Cambridgeshire, CHIO ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerquesesanger.ac.uk
Ch Oct 1, 2000 this sequence version replaced gi:10277922.
                                 U82207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence is not the entire insert of clone RP3-48221; It may be shorter because we sequence everlapping sections only once, except for a 100 base everlap.

The true left end of clone RP3-468B3 is at 51782 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Park Cancer institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ar/ox.de-droftnf
http://www.sanger.ar/ox.de-droftnf
http://www.sanger.ar/ox.de-droftnf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.samper.ac.uk/Tr/Sects/T_Seans/Wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         During sequence assembly data is compared from overlapping clones, where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The true right end of clone RP11-6H2O is at 100 in this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   feature key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kimberley, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniafa; Vertebrata; Eufeleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPC1-3"
11746 a 14123 c 13525 g 12487 t
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                                                                                                                                                                                                                                                                                                                   Competion live
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome-*6*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xrof-"taxon;9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone-"RP3 482021"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Nomo sapieus"
                                                                                                                                                                                                                                                                                                                                                74.6%; Score 19.4; DH 9; Length 51881; 95.2%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .51881
                             115297 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51881 bp
                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZNA
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                             Linear
                             HTG 40-AUG-2001
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Homo sapiens chromosome 10 clone CIT987SK-1119P3 map 10q25.1,

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SECHARAN
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                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC124782
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                                                                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GTGCTCTAATCTTTTCTCCTACCA 24
                  Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christop Cheveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R.
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (13-DDC-1996) Riginformatics Division, Genome Therapoutics Corporation 100 Braver Street, Waltham, MA 02154, USA On Dec 9, 1998 this sequence version replaced gi:1773045.
Note: Clone was sequenced in 1996 using Multiplex DNA Sequencing
                                                                                       Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Howie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Hurkett,C., Hurrell,K.L., Byrd,N.C.,
                                                                                                                                                                                                                                                                                                                                                                          HTG: HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegious clone CH230-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Davila, M.L., Davis, C., Davy Carroll, L., Dederich, D.A.,
                                                                                                                                                                MUZNY.D.M., Adams,C., Adio-Oduoia,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
                                                                                                                                                                                                                                                                     Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                   Battus norvegicus
                                                                                                                                                                                                                                                                                                                                                  Norway rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Du, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith,D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the gaps between them are based on estimates that have provided by the submitter This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by the finished sequence as soon as it is available and the accession number will be preserved.

1 115297: contig of 115297 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F ORBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 153909)
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/clone="CIT9878K-1119P3"
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/db_xref-"taxon:9606"
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                       Coyle, M.D., Dathorne, S.R., David, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -44703, *** SEQUENCING IN PROGRESS
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                                              Christopoulos, C
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COMMENT

arbitrary: Gaps between the couligs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence

as soon as it is available and the accession number will

1162: contig of 1162 bp in length

he preserved.

REFERENCE

AUTHORS

TITLE JOURNAL

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AUTHORS JOURNAL

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Natissour, F., Reify, S., Khan, U., Ning, I., Korvah, J., Kovar, C., Kratovic, J., Kurshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L. C., Lewis, L. C., Lewis, L. C., Lewis, L. C., Liu, J., Liu, W., Loulseqed, H., Liozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Mabeshwari, M., Mapua, P., Martin, R., Martindale, A., Martincy, E., Mincri, M., Mitchell, T., Mohabbat, K., Moyada, M., Mouris, S., Massey, H., Mawhincy, E., Mitchell, T., Mohabbat, K., Moyada, M., Mouris, S., Moser, M., Newison, J., Newtson, N., Nauyen, N., Nauyen, N., Nayer, N., Nauyen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (31 JUL 2002) Human Génôme Sequencing Center, Department of Molecular and Human Genetics, Baylor Collège of Medicine, one Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H. Tansey,J., Taylor,C., Taylor,T., Tellrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Veta,V., Villalon,D., Vinson,R., Wang,O., Wang,S., Ward Moore,S., Warren,R., Washington,C., Watlington,S. Williamson,A., Wieczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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    (see http://www.hys.lem.tmc.edu/dow-/Genbank_draft_data.html).
    NOTE: This is a 'working draft' sequence. It corrently
    consists of 38 contings. The true order of the pieces
    is not known and their order in this sequence record is

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                                                                                                                                                                                                                                          * NOTE: Estimated insert size may differ from sequence length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                               Chemistry: Dye-terminator Big Dye, 180% of reads Assembly program. Phrap: version 0.990329 Consensus quality: 124699 bases at least 040 Consensus quality: 130127 bases at least 030
                                                                                                                                                                                                                                                                                                                                                                         Consensus quality: 133717 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                        Cleveland, C.D., Cox.C., Nayle, M.D., Dathorum, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Pederich, D.A., Belancy, K.R., Delqado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Diaper, H., Dugan, Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Estaribart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Estaribart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Estaribart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Estaribart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Estaribart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Estaribart, C., Elhaj, C., Escotto, M., Estaribart, C., Elhaj, C., Elhaj,
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Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muzny, E.M., Adams, C., Adio Oduola, B., Ali osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, T.R., Ayele, M., Baunks, T., Barbaria, J., Benton, J., Bimoge, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Bires,M., Rojas,A., Rojubokan,T., Rolle,M., Rull,S., Savery,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gozzell J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N. C
Carron, T. F., Carter, M., Cavazos, S.R., Chacko, J., Chave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIIG;
                                                                    Weinstock, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris,C., Harris,K., Bart,M., Havlak,P., Hawes,A., Hernandez,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Falls,T., Ferraquto,D., Flagq,N., Ford,J., Foster,P., Frantz,P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (22-***(N-2002) Human Genome Sequencing Conter, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, "X 77030, HSA
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Worley, K.C.
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NOTE: This is a 'working draft' sequence. It currently
consists of 59 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the conditys are represented as
runs of N, but the exact sizes of the gaps are unknown.
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Contact: hgsc-help@bom.tmc.edu
Project Information
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                                                                                                                                         e mail: states@ibc.wustl.edu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (40-JAN-1998) Center for Genetics in Medicine, Box 8232, Washington University School of Medicine, 4566 Scott Avenue, St. Louis, Mo 64110, USA
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                                                                                                                                                             700 South Euclid Ave.
St. Louis, MO 63108 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poster City, CA 94404 USA e-mail: elison*qenseq.apldblo.com
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
L. (bases 1 to 160091)
                                                                                                                                                                                                             Washington University in St. Louis
                                                                                                                                                                                                                                  Institute for Biomedical Computing
                                                                                                                                                                                                                                                                David I States
                                                                                                                                                                                                                                                                                                                                                            e-mail: buddy*genetics.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buddy Brownstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               850 Lincoln Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Advanced Center for Genetic Technology,
Applied Biosystems Division of Perlin Elmer Corp.,
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as complicasions and repeats, all regions were covered by all least one plasmid subclone or more than one Mil subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger ac uk/mGr/chr10
RPII-211NI1 is from the library RPOLILL constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bitp://www.sampir.ac.ik/it/jests/__ispacs/wingep his segment was generated from part of bamberial clone contins of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lessuit, was continued by restriction diagrat. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL, Sw., SWISSPROT, Tr., TREMBL, Wp., WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found to the sequence schoolsston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 15, constructed by the samper centre chromosome 10 Mapping Group. Further intormation can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cambridgeshire, CBJO 1SA, UK. E-mail enquiries:
humquery?sanggr.ac.uk Clone requests. clonerequest/sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (15 NOV 2001) Wellcome Trust Sanger Institute, Hinzton,
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                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is the entire insert of clone RP11 211N11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VECTOR: pbAce3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buring sequence assembly data is compared from overlapping chomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Sep 12, 2001 this sequence version replaced gi:15041956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bakaryota: Metanda: Chordata, Cratiata, Vertebrata, Exteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Similarity 87.5%, Pred. No. 2.6e;02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 174776)
                                                                                                                  Consorvativo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See The
                                                                                                                                                                                                                                                          /db_xret-"taxon:9606"
/chromosome-"10"
                                                                                                                                                                                                                                                                                                                /close-"RFI1 211N11"
                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         .174776
                                                                                                                                             73.8%; Score 19.2; DB 9; Length 174776;
87.5%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mint semont conformation
                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen, G., Chen, E., Chen, C., Chondhry, I., Christopoulos, C.
Cleveland, C.P., Cry.c., Cryle, M.E., Catherine, S.E., Cavid, E.,
Davila, M.L., Davis, C., Davy-Carroll, L., Ding, Y., Dinh, H.H.,
Davila, M.L., Davis, C., Davy-Carroll, Ding, Y., Dinh, H.H.,
Davila, M.L., Davis, C., Davy-Carroll, Ding, Y., Dinh, H.H.,
Delancy, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Delancy, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Delancy, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraquito, D., Flagg, N., Ford, J., Escotto, M.,
Falls, T., Ferraquito, D., Flagg, N., Ford, J., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garror, T., Garra, N., Gill, P.,
Gorrell, J.H., Guovara, W., Gunarathie, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Harlis, C.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Harlis, C., Harris, C., Harris, C., Hame, T., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Tollvet, S., Hume, T., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Ning, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Louis, L.C., Lewis, L.,
Li, Li, L., Lichtarge, O., Licu, J., Licu, M., Louiseged, H.,
Li, Li, L., Lichtarge, O., Licu, J., Licu, M., Martindale, A.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E.,
Massey, E., Mawhiney, E., WcLeod, M.P., Meador, M., Morris, S.,
Moser, M., Neillo, N., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogub, M., Okwyon, G., Nguyen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oraquuye, N., Orledo P., Pape, A., Payron, B., Paper, T. Perez, T. Perez, T., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Pilves, M., Rojas, A., Rojubokan, I., Rolfe, M., Puiz, S., Savery, S., Scheret, S., Statt, G., Shan, H., Shan, Shaniry, H., Stope, H., Scodergren, E., Sonajke, T., Sparke, A., Tamerisa, A., Tamerisa, K., Tang, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, T., Taylor, T., Talirod, B., Thomas, M., Thomas, S., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williamson, A., Wiczyk, P., Washington, S., Worley, K., Wu, C., Wu, Y., F., Zhou, J., Zorriila, S., Noison, D., Weinstock, G., and Gibbs, R.
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                                                                                                                                                                                                                                                                                                                                                Submitted (29-33. 2002) Human Gename Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
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Mammalia; Eutheria; Redentia; Sciurognathi; Muridae; Muripae;
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65 unordered pieces.
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                                             Center clone name. CH230-9G8
                                                                                 Center project name: GDKY
                                                                                                                                                                        Web site: http://www.hgsc.bcm_tmc.edu/
Contact: hgsc-help@bcm_tmc_edu
                                                                                                                                                                                                                                                              Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submission
Summary Statistics
                                                                                                                 Project Intermation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Chavez.D.,
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arbitrary. Saps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is not known and their order in this sequence record is
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2340: gap of unknown length
3564: contig of 1224 bp in
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contig of 1862 t
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                                                                                                                                                                                                                                            Submitted (10 JUL 2002) Human Genome Sequencing Center, Department of Melecular and Human Schetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 9, 2002 this sequence version replaced gi:17941861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, one Baylor Plaza, Houston, TX 77030, USA
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Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flaqq,N., Ford,J., Foster,P., Frantz,P.,
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                                                                                                                                                                                                                                                                                                                                                                                       Worley, K.C.
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2 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                       Center clone name: CH230-4A13
                                                  Center project name.
                                                                                                       Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                               Center: Baylor College of Medicine Center code: HCM
                                                                                                                                  Web site: http://www.hqsc.bem.tmc.edu/

    Genome Center

                                                                            Project Information
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arbitrary. Gaps between the configs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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NOTE: This is a 'working draff' sequence it surrently consists of 94 contigs. The true order of the pieces is not known and their order in this sequence record is
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